GENETIC ANALYSES OF WASHINGTON STEELHEAD:

Preliminary results incorporating 36 new collections from 1995 and 1996

PROGRESS REPORT

Stevan R. Phelps, Steven A. Leider, Patrick L. Hulett,
Bruce M. Baker, and Thom Johnson

Washington Department of Fish and Wildlife
Fish Management Program
600 Capitol Way N
Olympia, WA 98501-1091

February 1997

q:\data\rbst\mega2\sthd977.txt

Chapter 4. Using collections from the 1970's to examine hatchery gene flow

Steelhead from Washington were one of the first salmonids to be studied for genetic population structure using protein electrophoresis. Some of the collections from Allendorf (1975) and the National Marine Fisheries Service occurred before locations were stocked heavily. Even though some locations were planted with hatchery fish before genetic sampling could occur, the amount of successful gene flow (introgression) over the last twenty years can be examined by comparing the genetic distance between the primary hatchery source, Chambers Creek Hatchery (CCH), and collections made approximately twenty years apart in similar locations. Thus, the genetic impacts due to the interbreeding of hatchery and wild fish as the result of the management practices of stocking hatchery origin steelhead into wild populations can be examined. One situation that would make the genetic distance between the hatchery and wild collections appear smaller is the sampling of progeny of hatchery X hatchery crosses that appear wild. If these fish do not interbreed, but are included in the collection, the genetic distance would appear smaller than its true value.

We compared the allele frequencies of CCH in Allendorf (1975) (CCH75) to the WDFW collection in 1993 (CCH93) to determine if they had changed significantly. One locus, *sMDH-B1,2**, had significantly more **78* alleles in the Allendorf data and in the overall test the two collections were significantly different also (χ^2 = 19.08, 7 df $p < 0.01$). If the allele frequencies at CCH had remained stable, then the CCH baseline used to compare with the wild steelhead collections would have mattered little. However, other genetic distance comparisons are possible. Another possibility would have been to compare all wild collections to CCH75 or compare the collections reported in Allendorf (1975) to the earlier CCH75 baseline data and the WDFW collections to CCH93. A quick browse of the genetic distances to CCH75 indicated that they were all slightly larger than the distances to CCH93, but the same patterns were present.

If the genetic distance between the Chambers Creek Hatchery collection made by WDFW in 1993 (CCH93) and the most recent collections made from 1993 - 1996 are smaller than the genetic distances between CCH93 and the collections made in the early 1970's, then it is likely that gene flow from the CCH strain into the wild population has been greater than the genetic drift or selective forces that are responsible for the differences. On the other hand, if the genetic distances between CCH93 and the 1990's collections are about the same or greater, then gene flow from CCH into those populations has been small relative to other forces shaping allele frequency characteristics of populations.

We chose wild-fish collections of Allendorf (1975) from four GDUs, Northern Puget Sound GDU 8 (six collections), North Coast GDU 9 (eight collections), South Coast GDU 1 (one collection), and Lower Columbia GDU 3 (two collections). Allendorf had no wild-fish collections from South Puget Sound GDU 2, and an insufficient number of comparable locations were present in the inland MAL GDUs.

We calculated the Cavalli-Sforza and Edwards (1967) chord distance based on the allele frequencies at seven loci between the CCH93 and collections in Allendorf (1975), and between CCH93 and WDFW collections from similar locations to those of Allendorf (1975) The seven loci (including one isolocus treated as a single locus) are: (*ADH*, G3PDH-1*, sIDHP-2*, LDH-B2*, sMDH-B1,2*, PGM-2*, sSOD-1**). We chose these seven loci because they were variable in many of the collections and the allelic data were comparable between the two data sets (alleles were pooled in the WDFW data to match the data format in Allendorf 1975).

The genetic distance comparisons between CCH93 and wild collections from Allendorf (1975) and WDFW varied between geographic regions (Table 4-1). In general, the WDFW Strait of Juan de Fuca collections are more similar to CCH93 than those of Allendorf, but many of the WDFW collections in other geographic areas had genetic distances equal to or greater than the distances between CCH93 and the earlier collections.

Northern Puget Sound GDU 8

We divided the collections from Allendorf (1975) in this GDU into four groups: Nooksack River, Skagit River (Sauk), Stillaguamish River summer-run and Stillaguamish River winter-run. All three of the WDFW collections from the Nooksack River had genetic distances that were larger than those from the Allendorf 1975 collection. Only one WDFW collection from the Skagit River, Cascade WR94, had a genetic distance that was smaller than the Sauk River collection from Allendorf (1975). The genetic distances of the three WDFW Deer Creek collections (1993-1995) to CCH93 were about equal to that for the Deer Creek collection from Allendorf (1975). The genetic distances to CCH93 in the winter-run collections from the Stillaguamish River were quite variable. We included WDFW collections from the Skykomish River also. A few of these distances were smaller than those from the Allendorf collections, but the remainder were about the same. The mainstem (MS) Skykomish River WR93 had the smallest genetic distance and it had been identified by Phelps et al. (1994) as having a large amount of introgression from CCH. From these comparisons it appears that gene flow from CCH into wild populations in this GDU has been minor and has not been widespread over the past twenty years.

\mega2\oldata\alcomp3.tbl

Table 4-1. A comparison of genetic distances (Cavalli-Sforza and Edwards chord) between collections of naturally produced steelhead and the WDFW 1993 Chambers Creek Hatchery collections. The before 1975 collections are from Allendorf (1975). Distances are based on seven polymorphic loci in common in the two studies.

Steelhead Collections and Genetic Distances

Before 1975		1993-1996	
Northern Puget Sound GDU 8			
SF Nooksack R WR	0.0850	SF Nooksack WR95	0.1092
		NF Nooksack WR95	0.1281
		SF Nooksack SR94	0.1200
Sauk R WR	0.0820	Sauk R WR94	0.0912
		Sauk SF S&W94	0.0892
		Suiattle R 94	0.1063
		Skagit R LMS 94	0.0816
		Skagit R UMS 94	0.0840
		Cascade 94	0.0755
		Finney Cr WR95	0.0843
Deer Cr A SR	0.1268	Deer Cr SR93	0.1300
		Deer Cr SR94	0.1267
		Deer Cr SR95	0.1319
Deer Cr B WR	0.0663	NF Stillagua WR93	0.0707
Stillagua A WR	0.0820	NF Skykomish WR93	0.0809
Stillagua B WR	0.0918	Pilchuck R WR93	0.0635
		Pilchuck R WR94	0.0910
		MS Skykomish WR93	0.0576
Snoqualmie R WR93	0.0649		
North Coast GDU 9			
Pysht R WR	0.0924	Pysht R WR94	0.0534
Twin R WR	0.0723	East Twin R WR94	0.0622
Hoko R WR	0.0899	Hoko R WR WR94	0.0787
Clallam R WR	0.0890	Lyre R WR95	0.0579
Morse Cr WR94	0.0590	Deep Cr WR96	0.0764
Sol Duc A WR	0.0707	Sol Duc R WR94	0.0771
Sol Duc B WR	0.0675	Sitkum R WR94	0.0791
Quinault R WR	0.0874	Bogachiel R WR94	0.0547
Dickey R WR	0.1586	Calawah R WR94	0.0773
		Hoh R WR95	0.0750
		Goodman Cr WR95	0.0622
		Hurst Cr WR95	0.0778
		Quinault NFH WR95	0.0639
		Quinault QIFH WR95	0.0965
South Coast GDU 1			
Wishkah R WR	0.1333	Humptulips WR94	0.0674
		Wynoochee WR94	0.0732
		Satsop R WR94	0.1168
		EF Satsop WR94	0.0991
		EF Humptulips WR94	0.0892
		WF Humptulips WR94	0.1004
		Stillman Cr WR94	0.1287
Lower Columbia GDU 3			
Gobar Cr WR	0.0405		
Kalama R WR	0.0747	Kalama R S&W94	0.0598
		EF Lewis WR96	0.0806
		SF Toutle WR96	0.0895
		EF Lewis SR96	0.0952
		Green Cowlitz WR96	0.0386
		Cedar Cr WR96 NFL	0.0585